```
=> fil reg; d que l2; d que l16
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DICTIONARY FILE UPDATES:    3 DEC 2001  HIGHEST RN 373353-24-3

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Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

L2          1117 SEA FILE=REGISTRY ABB=ON  CARCAR(CAG){7-12}CAA/SQSN

L2          1117 SEA FILE=REGISTRY ABB=ON  CARCAR(CAG){7-12}CAA/SQSN
L16            0 SEA FILE=REGISTRY ABB=ON  L2 AND SQL>29 AND SQL<46
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sequence length limited to 30-45 nucleotides

```
=> fil hcapl; d que l10; d que l13;d que l22; d que l26; s l10 or l13 or l22 or l26
FILE 'HCAPLUS' ENTERED AT 12:25:12 ON 04 DEC 2001
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FILE COVERS 1947 - 4 Dec 2001  VOL 135 ISS 24
FILE LAST UPDATED: 3 Dec 2001  (20011203/ED)

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in CA from 1947 to the present.  On April 22, 2001, bibliographic
information and abstracts were added for over 2.2 million references
published in CA from 1947 to 1966.

L2          1117 SEA FILE=REGISTRY ABB=ON  CARCAR(CAG){7-12}CAA/SQSN
L7           267 SEA FILE=HCAPLUS ABB=ON  L2
L8         38040 SEA FILE=HCAPLUS ABB=ON  MENTAL DISORDER+NT/CT
L9         19535 SEA FILE=HCAPLUS ABB=ON  MENTAL DISORDER+OLD/CT
```

Reg file answer set crossed into CAPLUS to get citations

Searched by Barb O'Bryen STIC 308-4291

```
L10          9 SEA FILE=HCAPLUS ABB=ON  L7 AND (L9 OR L8)

L2        1117 SEA FILE=REGISTRY ABB=ON  CARCAR(CAG){7-12}CAA/SQSN
L7         267 SEA FILE=HCAPLUS ABB=ON  L2
L11      75196 SEA FILE=HCAPLUS ABB=ON  POLYMORPH?/OBI
L13         10 SEA FILE=HCAPLUS ABB=ON  L11 (L) L7

L2        1117 SEA FILE=REGISTRY ABB=ON  CARCAR(CAG){7-12}CAA/SQSN
L7         267 SEA FILE=HCAPLUS ABB=ON  L2
L21        785 SEA FILE=HCAPLUS ABB=ON  HGT1 OR GT1 OR (HGT OR GT)(W)1
L22          2 SEA FILE=HCAPLUS ABB=ON  L7 AND L21

L2        1117 SEA FILE=REGISTRY ABB=ON  CARCAR(CAG){7-12}CAA/SQSN
L7         267 SEA FILE=HCAPLUS ABB=ON  L2
L11      75196 SEA FILE=HCAPLUS ABB=ON  POLYMORPH?/OBI
L23      11020 SEA FILE=HCAPLUS ABB=ON  REPETITIVE DNA+OLD/CT
L24       5696 SEA FILE=HCAPLUS ABB=ON  REPETITIVE DNA+NT/CT
L26         14 SEA FILE=HCAPLUS ABB=ON  L7 AND (L23 OR L24) AND L11

L30         24 L10 OR L13 OR L22 OR L26

=> d ibib ab hitrn l30 1-24

L30 ANSWER 1 OF 24  HCAPLUS  COPYRIGHT 2001 ACS
ACCESSION NUMBER:        2001:217589  HCAPLUS
DOCUMENT NUMBER:         134:220923
TITLE:                   Association of an X-chromosome dodecamer insertional
                         variant allele with mental retardation. [Erratum to
                         document cited in CA134:84488]
AUTHOR(S):               Philibert, R. A.; King, B. H.; Winfield, S.; Cook, E.
                         H.; Lee, Y.-H.; Stubblefield, B.; Damschroder-
                         Williams, P.; Dea, C.; Palotie, A.; Tengstrom, C.;
                         Martin, B. M.; Ginns, E. I.
CORPORATE SOURCE:        Clinical Neuroscience Branch, National Institute of
                         Mental Health, Bethesda, MD, 20892, USA
SOURCE:                  Mol. Psychiatry (1999), 4(2), 197
                         CODEN: MOPSFQ; ISSN: 1359-4184
PUBLISHER:               Stockton Press
DOCUMENT TYPE:           Journal
LANGUAGE:                English
AB   The sequences of the reverse primer on page 304 and Fig. 1 were incorrect.
     The correct sequence for the reverse primer is as follows (5' to 3'):
     GGGCTGTAGTCCAGCAGCTACCTG.  The correct Fig. 1 is given.
IT   228686-91-7, GenBank AF132033
     RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
     BPR (Biological process); PRP (Properties); BIOL (Biological study); OCCU
     (Occurrence); PROC (Process)
        (nucleotide sequence; assocn. of X-chromosome dodecamer insertional
        variant allele of OPA-contg. protein with mental retardation in humans
        in relation to sequences for human and mouse (Erratum))
IT   222771-68-8, GenBank AF071311
     RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
     PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
        (nucleotide sequence; assocn. of X-chromosome dodecamer insertional
        variant allele of OPA-contg. protein with mental retardation in humans
```

se registry to match notation to sequence (printed after all citations)

in relation to sequences for human and mouse (Erratum))

IT **212951-28-5**, GenBank AF071309
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; assocn. of X-chromosome dodecamer insertional variant allele of OPA-contg. protein with mental retardation in humans in relation to sequences for human and mouse (Erratum))

L30 ANSWER 2 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:707338 HCAPLUS
DOCUMENT NUMBER: 133:291967
TITLE: Single nucleotide polymorphisms in coding regions of human genes and primers/probes and methods for detection thereof
INVENTOR(S): Altshuler, David; Cargill, Michele; Daley, George Q.; Ireland, James S.; Lander, Eric S.; Lipshutz, Robert J.; Patil, Nila; Sklar, Pamela
PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA; Affymetrix, Inc.
SOURCE: PCT Int. Appl., 216 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000058519	A2	20001005	WO 2000-US8440	20000330

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-127248 P 19990331
AB The invention provides nucleic acid segments of the human genome, particularly nucleic acid segments from the coding region of a gene, including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking or contg. these sites are also provided. The nucleic acids, primers and probes are used in applications such as phenotype correlations, forensics, paternity testing, medicine and genetic anal. Thus, SNPs were identified in 106 genes relevant to cardiovascular disease, endocrinol., and neuropsychiatry by screening an av. of 114 independent alleles using two independent screening methods. To ensure high accuracy, all reported SNPs were confirmed by DNA sequencing. A total of 545 SNPs were identified, including 395 coding region SNPs (cSNPs) divided roughly equally between those causing synonymous and nonsynonymous changes. The cSNPs most likely to influence disease, those that alter the amino acid sequence of the encoded protein, showed strikingly different properties: they occurred at a lower rate and with lower allele frequencies.
IT **300736-73-6 300736-74-7**
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(nucleotide sequence; single nucleotide **polymorphisms** in coding regions of human genes and primers/probes and methods for detection thereof)

L30 ANSWER 3 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:691680 HCAPLUS

DOCUMENT NUMBER: 134:290973
TITLE: Identification and characterization of the miniature pig Huntington's disease gene homolog: evidence for conservation and **polymorphism** in the CAG triplet repeat
AUTHOR(S): Matsuyama, Noriko; Hadano, Shinji; Onoe, Kyuichiro; Osuga, Hitoshi; Showguchi-Miyata, Junko; Gondo, Yoichi; Ikeda, Joh-E.
CORPORATE SOURCE: Department of Neurobiology, SLA Research, Inc., Bohseidai, Isehara, Kanagawa, 259-1193, Japan
SOURCE: Genomics (2000), 69(1), 72-85
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Huntington's disease (HD) is assocd. with a significant expansion of a CAG trinucleotide repeat, which results in a lengthened polyglutamine tract in the single gene product, huntingtin, on human 4p16.3. We isolated cDNA clones that encompassed the entire coding sequence of the miniature pig HD gene (Sus HD) from two porcine testis cDNA libraries. The cDNA contig revealed a 12,749-nucleotide transcript coding for a 345-kDa protein (3139 amino acid residues), which exhibited 96% peptide sequence homol. to human huntingtin. Northern blot anal. revealed that the Sus HD gene was ubiquitously expressed as two large transcripts of approx. 11 and 13 kb in size in all the tested tissues, much like the human HD gene. The CAG trinucleotide repeat was found to be interrupted by CAA triplets and to encode 17 or 18 consecutive glutamine residues. In our lab. stock of miniature pig, three allotypes in the triplet repeat sequence were found. Thus, the Sus HD gene closely resembles its human counterpart in terms of sequence and expression pattern. In particular, human-miniature pig similarities in the normal length of the CAG triplet repeat as well as its repeat-no. polymorphism may indicate that miniature pig would provide a good animal model for Huntington's disease. (c) 2000 Academic Press.
IT **224698-75-3**, GenBank AB016793 **224698-76-4**, GenBank AB016794
RL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)
(nucleotide sequence; characterization of the miniature pig Huntington's disease gene homolog and evidence for conservation and **polymorphism** in the CAG triplet repeat)
REFERENCE COUNT: 51
REFERENCE(S): (1) Altschul, S; Nucleic Acids Res 1997, V25, P3389 HCAPLUS
(2) Ambrose, C; Somat Cell Mol Genet 1994, V20, P27 HCAPLUS
(3) Andrade, M; Nat Genet 1995, V11, P115 HCAPLUS
(4) Andrew, S; Hum Mol Genet 1994, V3, P65 HCAPLUS
(5) Andrew, S; Hum Mol Genet 1997, V6, P2005 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 4 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:573324 HCAPLUS
DOCUMENT NUMBER: 134:84488
TITLE: Association of an X-chromosome dodecamer insertional variant allele with mental retardation
AUTHOR(S): Philibert, R. A.; King, B. H.; Winfield, S.; Cook, E. H.; Lee, Y-H.; Stubblefield, B.; Damschroder-Williams, P.; Dea, C.; Palotie, A.; Tengstrom, C.; Martin, B. M.; Ginns, E. I.
CORPORATE SOURCE: Clinical Neuroscience Branch, National Institute of Mental Health, Bethesda, MD, 20892, USA
SOURCE: Mol. Psychiatry (1998), 3(4), 303-309
CODEN: MOPSFQ; ISSN: 1359-4184

Searched by Barb O'Bryen STIC 308-4291

PUBLISHER: Stockton Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Mental retardation is a prominent feature of many neurodevelopmental syndromes. In an attempt to identify genetic components of these illnesses, the authors isolated and sequenced a large no. of human genomic cosmid inserts contg. large trinucleotide repeats. One of these cosmids, Cos-4, maps to the X-chromosome and contains the sequence of a 7.3-kb mRNA. Initial polymorphism anal. across a region of repetitive DNA in this gene revealed a rare 12-bp exonic variation (.mchlt.1% in non-ill males) having an increased prevalence in non-Fragile X males with mental retardation (4%). This variant was not present in the highly conserved mouse homolog that has 100% amino acid identity to the human sequence near the polymorphism. Subsequent screening of two addnl. independent cohorts of non-Fragile X mentally retarded patients and ethnically matched controls demonstrated an even higher prevalence of the 12-bp variant in males with mental retardation (8%, and 14%) vs. the controls. Multivariate anal. was conducted in an effort to identify other phenotypic components in affected individuals, and the findings suggested an increased incidence of histories of hypothyroidism and treatment with antidepressants. The authors conclude that the presence of this 12-bp variant confers significant susceptibility for mental retardation.

IT **228686-91-7**, GenBank AF132033
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence); BPR (Biological process); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(nucleotide sequence; assocn. of X-chromosome dodecamer insertional variant allele of OPA-contg. protein with mental retardation in humans in relation to sequences for human and mouse)

IT **222771-68-8**, GenBank AF071311
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; assocn. of X-chromosome dodecamer insertional variant allele of OPA-contg. protein with mental retardation in humans in relation to sequences for human and mouse)

IT **212951-28-5**, GenBank AF071309
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; assocn. of X-chromosome dodecamer insertional variant allele of OPA-contg. protein with mental retardation in humans in relation to sequences for human and mouse)

REFERENCE COUNT: 27
REFERENCE(S):
(1) Altschul, S; J Mol Biol 1990, V215, P403 HCAPLUS
(3) Brown, W; JAMA 1993, V270, P1569 HCAPLUS
(5) Duboule, D; Mol Cell Biol 1987, V7, P2003 HCAPLUS
(6) Fransen, E; Eur J Hum Genet 1995, V3, P273 HCAPLUS
(7) Gecz, J; Hum Mol Genet 1997, V6, P435 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 5 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:97904 HCAPLUS
DOCUMENT NUMBER: 132:289469
TITLE: A preliminary gene map for the Van der Woude syndrome critical region derived from 900 kb of genomic sequence at 1q32-q41
AUTHOR(S): Schutte, Brian C.; Bjork, Bryan C.; Coppage, Kevin B.; Malik, Margaret I.; Gregory, Simon G.; Scott, Deborah J.; Brentzell, Luci M.; Watanabe, Yoriko; Dixon, Michael J.; Murray, Jeffrey C.
CORPORATE SOURCE: Department of Pediatrics, University of Iowa, Iowa City, IA, 52242, USA
SOURCE: Genome Res. (2000), 10(1), 81-94
CODEN: GEREFS; ISSN: 1088-9051

Searched by Barb O'Bryen STIC 308-4291

PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Van der Woude syndrome (VWS) is a common form of syndromic cleft lip and palate and accounts for .apprx.2% of all cleft lip and palate cases. Distinguishing characteristics include cleft lip with or without cleft palate, isolated cleft palate, bilateral lip pits, hypodontia, normal intelligence, and an autosomal-dominant mode of transmission with a high degree of penetrance. Previously, the VWS locus was mapped to a 1.6-cM region in 1q32-q41 between DIS491 and DIS205, and a 4.4-Mb contig of YAC clones of this region was constructed. In the current investigation, gene-based and anonymous STSs were developed from the existing phys. map and were then used to construct a contig of sequence-ready bacterial clones across the entire VWS crit. region. All STSs and BAC clones were shared with the Sanger Center, which developed a contig of PAC clones over the same region. A subset of 11 clones from both contigs was selected for high-throughput sequence anal. across the .apprx.1.1-Mb region; all but two of these clones have been sequenced completely. Over 900 kb of genomic sequence, including the 350-kb VWS crit. region, were analyzed and revealed novel polymorphisms, including an 8-kb deletion/insertion, and revealed 4 known genes, 11 novel genes, 9 putative genes, and 3 pseudogenes. The positional candidates LAMB3, GOS2, HIRF6, and HSD11 were excluded as the VWS gene by mutation anal. A preliminary gene map for the VWS crit. region is as follows: CEN-VWS33-VWS34-D1S491-VWS1-VWS19-LAMB3-GOS2-VWS26-VWS25-HSD11-ADORA2BP-VWS17-VWS14-HIRF6-VWS2-VWS18-D1S205-VWS23-VWS20-VWS30-VWS31-VWS35-VWS37-VWS38-HIPP-RNASEH1P-VWS40-VWS42-VWS41-TEL. The data provided here will help lead to the identification of the VWS gene, and this study provides a model for how labs. that have a regional interest in the human genome can contribute to the sequencing efforts of the entire human genome.
IT **225458-12-8**, GenBank AL035408
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; STS content and sequence anal. of contigs spanning VWS region at human 1q32-q41 identifies 11 novel genes and 3 pseudogenes)
REFERENCE COUNT: 81
REFERENCE(S):
(1) Aberdam, D; Mamm Genome 1994, V5, P229 HCAPLUS
(2) Adachi, M; Biochem Biophys Res Commun 1992, V186, P1607 HCAPLUS
(3) Ahmad, N; Proc Natl Acad Sci 1991, V88, P6624 HCAPLUS
(4) Altschul, S; J Mol Biol 1990, V215, P403 HCAPLUS
(5) Becker, W; Prog Nucleic Acid Res Mol Biol 1999, V62, P1 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 6 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:811376 HCAPLUS
DOCUMENT NUMBER: 132:45827
TITLE: YAC fragmentation vectors using short triplet repeats as the target sequence for homologous recombination and their uses in phys. mapping human genome
INVENTOR(S): Del-Favero, Jurgen; Van Broeckhoven, Christine
PATENT ASSIGNEE(S): Vlaams Interuniversitair Instituut Voor Biotechnologie VZW, Belg.
SOURCE: PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9966059	A1	19991223	WO 1999-EP4106	19990611
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9945131	A1	20000105	AU 1999-45131	19990611
PRIORITY APPLN. INFO.:			EP 1998-201976	19980612
			WO 1999-EP4106	19990611

AB Novel vectors for liberation of subsequences from yeast artificial chromosomes (YACs), called fragmentation vectors, use short triplet repeats as the target sequence for homologous recombination to ext. sequences from the larger clone. These vectors can be used in large-scale mapping and sequencing projects. The new vectors have one telomere, a selectable marker (Lys2) and one short triplet repeats as the target sequence for homologous recombination, either with or without a centromere. These vectors allow direct acentric and centric fragmentation of yeast artificial chromosomes (YACs) and selection of fragmented YACs contg. triplet repeats sequence in yeast strain AB1380. High recombination efficiencies were obtained in fragmentations of YAC clones contg. SCA7 (spinocerebellar ataxia type 7) gene or SPG4 locus (one of loci for dominant spastic paraplegia) using vectors with a low-copy no. of CAG or CTG triplet repeats. (SCA7 is the causative agent for autosomal dominant cerebellar ataxia with retinal degeneration if 10 of CAG repeats in its exon I expanded to 38). Several sets of fragmented clones were obtained according to their final sizes and all clones with the same size represented a sequence-specific recombination event. Two vectors with a short sequence of CGG or CCG repeats were shown to have even higher recombination efficiency than those with CAG or CTG repeats. These repeats-based fragmentation vectors are esp. useful to discover the abnormality in the polymorphism of short triplet repeats in the flanking regions of specific human genes which might play a role in its aberrant expression and assocd. disorders.

IT **252869-02-6**, 3: PN: WO9966059 SEQID: 3 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; yAC fragmentation vectors using short triplet repeats as the target sequence for homologous recombination and their uses in phys. mapping human genome)

REFERENCE COUNT: 7

REFERENCE(S):

(1) Cook, G; Nucleic Acids Research 1996, V24(8), P1585 HCAPLUS
(2) Del-Favero, J; Gene An International Journal on Genes and Genomes 1999, V229(1-2), P193 HCAPLUS
(3) Hamer, L; Proceedings of the National Academy of Sciences 1995, V92, P11706 HCAPLUS
(4) Heard, E; Nucleic Acids Research 1994, V22(10), P1830 HCAPLUS
(5) Heus, J; Genome Research 1997, V7(6), P657 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 7 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:708954 HCAPLUS
DOCUMENT NUMBER: 131:333051
TITLE: Identification and detection of **polymorphisms** in the PCTG4 region of human chromosome Xq13 assocd. with neuropsychiatric disorders
INVENTOR(S): Philibert, Robert A.; Ginns, Edward I.

Searched by Barb O'Bryen STIC 308-4291

PATENT ASSIGNEE(S): United States Department of Health and Human Services, USA; University of Iowa Research Foundation
SOURCE: PCT Int. Appl., 100 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9955915	A2	19991104	WO 1999-US9365	19990429
WO 9955915	A3	20000309		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9937730	A1	19991116	AU 1999-37730	19990429

PRIORITY APPLN. INFO.: US 1998-83465 P 19980429
WO 1999-US9365 W 19990429

AB Claimed are nucleic acid sequences within the q13 region of the X chromosome having polymorphisms assocd. with neuropsychiatric disorders and assocd. conditions. One polymorphism occurs within the coding region of the HOPA gene and introduces a four amino acid insertion into a putative OPA domain, a domain which has been shown to be involved in tissue specific expression. Compns. including nucleic acids having these polymorphisms and antibodies to polymorphic regions within proteins encoded in the PCTG4 region are provided. Methods of using the information and nucleic acid sequences disclosed herein for the diagnosis and assessment of pathologies assocd. with neuropsychiatric disorders and assocd. conditions are also provided.

IT **249928-10-7 249928-12-9**
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); BOC (Biological occurrence); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; identification and detection of **polymorphisms** in PCTG4 region of human chromosome Xq13 assocd. with neuropsychiatric disorders)

IT **249726-48-5**, PN: WO9955915 FIG: 5 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; identification and detection of **polymorphisms** in the PCTG4 region of human chromosome Xq13 assocd. with neuropsychiatric disorders)

L30 ANSWER 8 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:642896 HCAPLUS
DOCUMENT NUMBER: 132:161851
TITLE: The genomic structure and developmental expression patterns of the human OPA-containing gene (HOPA)
AUTHOR(S): Philibert, Robert A.; Winfield, Suzanne L.; Damschroder-Williams, Pat; Tengstrom, Carola; Martin, Brian M.; Ginns, Edward I.
CORPORATE SOURCE: Department of Psychiatry, University of Iowa, Iowa City, IA, 52242-1000, USA
SOURCE: Hum. Genet. (1999), 105(1-2), 174-178
CODEN: HUGEDQ; ISSN: 0340-6717
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal

LANGUAGE: English

AB We detd. the genomic organization of the human OPA-contg. gene (HOPA) and characterized its developmental expression. The gene encoding HOPA, which contains a rare polymorphism tightly assocd. with non-specific mental retardation, is 25 kb in length and consists of 44 exons. A promoter scan anal. demonstrates two possible transcription initiation sites without TATA boxes upstream from the putative translation initiation start site. Several informative polymorphisms are evident in the sequence including a large pentanucleotide repeat. Northern blot anal. of the gene transcript and its murine orthologue, MOPA-1, demonstrates that only one transcript is expressed throughout the soma and the CNS, and that the transcript is highly expressed during early fetal development. We conclude that the delineation of the function of the HOPA gene locus merits further study.

IT **228686-91-7**, GenBank AF132033
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; genomic structure, DNA sequence, genetic **polymorphism** and developmental expression patterns of the human OPA-contg. gene (HOPA))

REFERENCE COUNT: 17

REFERENCE(S):
(2) Altschul, S; J Mol Biol 1990, V215, P403 HCAPLUS
(4) Grabowski, D; Biochim Biophys Acta 1991, V1090, P115 HCAPLUS
(5) Ito, M; Mol Cell Biol 1999, V3, P361 HCAPLUS
(7) Margolis, R; Hum Genet 1997, V100, P114 HCAPLUS
(8) Nagase, T; DNA Res 1996, V3, P321 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 9 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:594965 HCAPLUS
DOCUMENT NUMBER: 131:223513
TITLE: Proapoptotic peptides, dependence polypeptides and methods of use
INVENTOR(S): Bredesen, Dale E.; Rabizadeh, Shahrooz
PATENT ASSIGNEE(S): The Burnham Institute, USA
SOURCE: PCT Int. Appl., 199 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9945944	A1	19990916	WO 1999-US5250	19990311
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6235872	B1	20010522	US 1998-41886	19980312
AU 9930765	A1	19990927	AU 1999-30765	19990311
EP 1061935	A1	20001227	EP 1999-912380	19990311
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1998-41886 A 19980312
WO 1999-US5250 W 19990311

AB The present invention provides substantially pure proapoptotic dependence peptides. The peptides consist substantially of the sequence of an active dependence domain selected from the group of dependence polypeptides consisting of the neurotrophin receptor p75NTR, androgen receptor, DCC, huntingtin polypeptide, Machado-Joseph disease gene product, SCA1, SCA2, SCA6 and atrophin-1 polypeptide. Substantially pure proapoptotic dependence peptides include SATLDALLAALRRI (SEQ ID NO:3), Q14 (SEQ ID NO:7), SATLDALLAALGGI (SEQ ID NO:4), SATLDALLAALRGI (SEQ ID NO:5),

SATLQALLAALRRI (SEQ ID NO:6), tat-GG-SATLDALLAALRRI (SEQ ID NO:37) and tat-GG-Q14 (SEQ ID NO:36). The invention also provides a method of increasing cell survival. The method consists of inhibiting the function of an active proapoptotic dependence domain. A method of increasing cell survival consisting of preventing or reducing the rate of formation of an active proapoptotic dependence domain is also provided. The invention further provides a method of identifying compds. which prevent or inhibit apoptosis. The method consists essentially of administering a test compd. to a cell undergoing dependence domain mediated apoptosis, and detg. whether the compd. increases cell survival. A method of reducing the severity of a proapoptotic dependence domain mediated pathol. condition is also provided. The method consists of inhibiting the function of an active dependence domain. Addnl. provided is a method of reducing the severity of a pathol. condition mediated by unregulated cell growth. The method consists of cytoplasmically administering a proapoptotic dependence peptide.

IT **140026-49-9**, PN: WO9945943 SEQID: 10 unclaimed DNA
244017-45-6, PN: WO9945943 SEQID: 14 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; proapoptotic peptides, dependence polypeptides and methods of use)

REFERENCE COUNT: 4
REFERENCE(S):
(1) Goldberg, Y; Nature Genetics 1996, V13, P442 HCAPLUS
(2) Hileman, M; FEBS Letters 1997, V415, P145 HCAPLUS
(3) Imbert, G; Nature Genetics 1996, V14, P285 HCAPLUS
(4) Nishimoto; JP 02069665 A 1990 HCAPLUS

L30 ANSWER 10 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:549370 HCAPLUS
DOCUMENT NUMBER: 131:168354
TITLE: The potassium ion-channel responsible for the slow depolarizing current Ih and cDNAs encoding it
INVENTOR(S): Baumann, Arnd; Bonigk, Wolfgang; Gauss, Renate; Scholten, Alexander; Seifert, Reinhard; Kaupp, Benjamin
PATENT ASSIGNEE(S): Forschungszentrum Julich G.m.b.H., Germany
SOURCE: PCT Int. Appl., 82 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9942574	A1	19990826	WO 1999-EP942	19990212
W: JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
DE 19806581	A1	19991021	DE 1998-19806581	19980217
EP 1054963	A1	20001129	EP 1999-907550	19990212
R: CH, DE, DK, FR, GB, LI, NL, SE				

PRIORITY APPLN. INFO.: DE 1998-19806581 A 19980217
WO 1999-EP942 W 19990212

AB CDNAs for the potassium channel that is responsible for the slow depolarizing current Ih that plays a role in many processes including in the heart pacemaker system and rod photoreception are cloned from a no. of animals. CDNAs are obtained from human, rat, cattle, Drosophila melanogaster, and a sea urchin. The protein or the cDNA may be of use in the diagnosis, prophylaxis, or treatment of disease, esp. cardiovascular disease. DNAs were cloned by PCR using degenerate primers. Identity of the clones was identified electrophysiol. upon expression of the cDNA in

HEK293 cells.

IT **237745-29-8**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; potassium ion-channel responsible for slow depolarizing current Ih and cDNAs encoding it)

REFERENCE COUNT: 5
REFERENCE(S):
(1) Gauss, R; Nature 1998, V393, P583 HCAPLUS
(2) Hillier, L; Homo sapiens cDNA clone similar to DmCNGC protein-fruit fly
(3) Ludwig, A; Nature 1998, V393, P587 HCAPLUS
(4) Santoro, B; Cell 1998, V93, P717 HCAPLUS
(5) Santoro, B; Proceedings of the National Academy of Sciences of USA 1997, V94, P14815 HCAPLUS

L30 ANSWER 11 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:421768 HCAPLUS
DOCUMENT NUMBER: 131:68556
TITLE: cDNAs for SH3 domain-containing cyclic nucleotide-gated ion channels of the mammalian brain and heart
INVENTOR(S): Kandel, Eric R.; Santoro, Bina; Bartsch, Dusan; Siegelbaum, Steven; Tibbs, Gareth; Grant, Seth
PATENT ASSIGNEE(S): The Trustees of Columbia University in the City of New York, USA
SOURCE: PCT Int. Appl., 214 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9932615	A1	19990701	WO 1998-US27630	19981223
W: AU, CA, JP, MX				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9920160	A1	19990712	AU 1999-20160	19981223
EP 1042460	A1	20001011	EP 1998-964946	19981223
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.:
US 1997-997685 A 19971223
US 1998-86436 A 19980528
WO 1998-US27630 W 19981223

AB CDNAs for cyclic nucleotide gated ion channels of the mammalian brain and heart are cloned and characterized. The channels may play important roles in key neurol. functions and may be useful as targets for pharmaceuticals and methods for screening for effectors of the protein or of gene expression are described. Methods that are generally applicable to identifying genes for these channels are described. The first of these channels (mBCNG-1) was first identified in mouse as proteins interacting with the neuronal cell-specific splicing isoform of N-src via the SH3 domain showing some similarity to the Eag and H-erg ion channels and appear to constitute a new branch of the voltage-gated potassium channel superfamily. The protein was detected immunochem. in the brain, esp. the cerebral cortex, hippocampus and cerebellum. The protein was found in the dendrites of pyramidal cells and the axons of basket cells. Using the first clone to obtain related sequences identified several homologs with different patterns of tissue distribution. BLAST searching identified homologous ESTs in mouse and human. Expression of the mBCNG-1 clone in Xenopus oocytes led to the development of a pacemaker-like function that used potassium and sodium to carry the current that was sensitive to

cesium blockage.

IT **201441-24-9**, GenBank AF028737
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; cDNAs for SH3 domain-contg. cyclic nucleotide-gated ion channels of mammalian brain and heart)

REFERENCE COUNT: 8
REFERENCE(S):
(1) Biel; J Biol Chem 1996, V15(11), P6349
(3) Pedarzani; Proc Natl Acad Sci USA 1995, V92, P11716 HCAPLUS
(4) Santoro; Cell 1998, V93, P717 HCAPLUS
(7) Wang; J Neuroscience 1997, V17(3), P882 HCAPLUS
(8) Williamson; Nature 1980, P214 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 12 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:223024 HCAPLUS
DOCUMENT NUMBER: 130:263145
TITLE: **Polymorphic** CAG repeat-containing gene and its association with schizophrenia
INVENTOR(S): Rouleau, Guy A.; Joober, Ridha; Benkelfat, Chawki
PATENT ASSIGNEE(S): McGill University, Can.
SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9915639	A1	19990401	WO 1998-CA884	19980918
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9891495	A1	19990412	AU 1998-91495	19980918
EP 1015574	A1	20000705	EP 1998-943607	19980918
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001517432	T2	20011009	JP 2000-512932	19980918

PRIORITY APPLN. INFO.: CA 1997-2216057 A 19970919
WO 1998-CA884 W 19980918

AB The present invention relates to **hGT1** gene, a polymorphic CAG repeat-contg. gene, and its potential uses for the diagnosis, prognosis and treatment of psychiatric diseases such as schizophrenia. An aim of this invention is to detect assocn. between allelic variants of CAG repeat-contg. genes and schizophrenia or its phenotypic variability with respect to long term response to neuroleptic medication. CAG repeat allelic variants were compared between three groups of schizophrenic patients, and the results in accordance with this invention show that short CAG repeat allelic variants of the **hGT1** gene are assocd. with schizophrenia irresp. of neuroleptic response, and CAG repeat length is strongly correlated with the overall pattern of severity of the disease.

IT **221891-82-3**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(nucleotide sequence; **polymorphic** cag repeat-contg. gene and its assocn. with schizophrenia)
REFERENCE COUNT: 8
REFERENCE(S): (2) Joober, R; AMERICAN JOURNAL OF MEDICAL GENETICS 1996, V67(2), P235 MEDLINE
(3) Maciel, P; AMERICAN JOURNAL OF HUMAN GENETICS 1995, V57(1), P54 HCAPLUS
(4) Philibert, R; EUROPEAN JOURNAL OF HUMAN GENETICS 1998, V6(1), P89 HCAPLUS
(7) Univ British Columbia; WO 9718825 A 1997 HCAPLUS
(8) Univ Minnesota; WO 9501437 A 1995 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 13 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:155768 HCAPLUS
DOCUMENT NUMBER: 131:54534
TITLE: The characterization and sequence analysis of thirty CTG-repeat containing genomic cosmid clones
AUTHOR(S): Philibert, Robert A.; Horelli-Kuitunen, Nina; Robb, Adelaide S.; Lee, Yu-Hsien; Long, Robert T.; Damschroder-Williams, Patricia; Martin, Brian M.; Brennan, Miles B.; Palotie, Aarno; Ginns, Edward I.
CORPORATE SOURCE: Clinical Neuroscience Branch, National Institute of Mental Health, National Institutes of Health, Bethesda, MD, 20892-4405, USA
SOURCE: Eur. J. Hum. Genet. (1998), 6(1), 89-94
CODEN: EJHGEU; ISSN: 1018-4813
PUBLISHER: Stockton Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have systematically isolated and characterized DNA contg. large CTG (n > 7) repeats from a human cosmid genomic DNA library. Using a CTG10 probe, more than 100 cosmid clones were identified, and 30 of these have been extensively characterized. The sequenced cosmids contain repeats that are between three and 19 perfect units (av. 10 perfect repeats). The cosmids map to at least 12 different chromosomes. Sequence anal. of flanking regions suggests that more than one third of the repeats occur in exons, and many share strong sequence identity with databank sequences, including the gene involved in dentatorubral pallidoluysian atrophy (DRPLA). Genotyping of human DNA samples demonstrates that more than half of the repeats are polymorphic. This and similar collections of clones contg. trinucleotide repeats should aid in the identification of genes that may contain expansions of trinucleotide repeats involved in human disease.
IT **206322-20-5**, GenBank AF021105 **206322-26-1**, GenBank AF021111
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; characterization and sequence anal. of thirty CTG-repeat contg. genomic cosmid clones)
REFERENCE COUNT: 29
REFERENCE(S): (1) Altschul, S; J Mol Biol 1990, V215, P403 HCAPLUS
(2) Armour, J; Hum Mol Genet 1994, V3, P599 HCAPLUS
(3) Buxton, J; Nature 1992, V355, P547 HCAPLUS
(4) Gastier, J; Genomics 1996, V32, P75 HCAPLUS
(5) Gastier, J; Hum Mol Genet 1995, V4, P1829 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 14 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:571382 HCAPLUS
DOCUMENT NUMBER: 129:311468
TITLE: Length polymorphism in a CAG-rich coding region of the canine dentatorubro-pallidoluysian atrophy (DRPLA)

gene
AUTHOR(S): Chen, Y-W.; Liu, P-C.; Shibuya, H.; O'Brien, D. P.; Lubahn, D. B.; Johnson, G. S.
CORPORATE SOURCE: Departments of Veterinary Pathobiology, University of Missouri, Columbia, MO, 65211, USA
SOURCE: Anim. Genet. (1998), 29(3), 241
CODEN: ANGEE3; ISSN: 0268-9146
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A 0.37 kb amplicon from canine dentatorubro-pallidoluysian atrophy (DRPLA) gene was sequenced, which included a polymorphic CAG-rich region.
IT **200048-64-2**, GenBank AF030429
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; length **polymorphism** in CAG-rich coding region of canine dentatorubro-pallidoluysian atrophy (DRPLA) gene)

L30 ANSWER 15 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:332176 HCAPLUS
DOCUMENT NUMBER: 129:91216
TITLE: A novel long and unstable CAG/CTG trinucleotide repeat on chromosome 17q
AUTHOR(S): Ikeuchi, Takeshi; Sanpei, Kazuhiro; Takano, Hiroki; Sasaki, Hidenao; Tashiro, Kunio; Cancel, Geraldine; Brice, Alexis; Bird, Thomas D.; Schellenberg, Gerry D.; Pericak-Vance, Margaret A.; Welsh-Bohmer, Kathleen A.; Clark, Lorraine N.; Wilhelmsen, Kirk; Tsuji, Shoji
CORPORATE SOURCE: Department of Neurology, Brain Research Institute, Niigata University, Niigata, 951, Japan
SOURCE: Genomics (1998), 49(2), 321-326
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Using the direct identification of repeat expansion and cloning technique, a novel long CAG/CTG trinucleotide repeat was cloned on chromosome 17. Using radiation hybrid panels, the CAG/CTG repeat was mapped to chromosome 17q. The CAG/CTG repeat is highly polymorphic, with a heterozygosity of 85%, and exhibits a bimodal distribution (allele S, 10-26 repeat units, and allele L, 50-92 repeat units). The CAG/CTG repeat of allele L exhibited intergenerational instabilities, which are more prominent in maternal transmission than in paternal transmission. Analyses of Northern blot and RT-PCR indicate that the repeat is transcribed. Although the size of the CAG/CTG repeat of allele L is within the range of the expanded CAG repeat of disease-causing genes, the authors did not detect any assocn. of allele L with various neurodegenerative diseases, including frontotemporal dementia and parkinsonism, mapped to 17q21-q23.
IT **208229-17-8**, GenBank AB009843
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; sequence of a novel long and unstable CAG/CTG trinucleotide repeat on human chromosome 17q)

L30 ANSWER 16 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:735887 HCAPLUS
DOCUMENT NUMBER: 128:21486
TITLE: The huntingtin gene IT15 affected by a trinucleotide expansion mutation in Huntington's disease and its uses
INVENTOR(S): MacDonald, Marcy E.; Ambrose, Christine M.; Duyao, Mabel P.; Gusella, James F.
PATENT ASSIGNEE(S): General Hospital Corp., USA

Searched by Barb O'Bryen STIC 308-4291

SOURCE: U.S., 112 pp. Cont.-in-part of U.S. Ser. No. 85,000, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5686288	A	19971111	US 1994-246982	19940520
CA 2116280	AA	19940906	CA 1994-2116280	19940223
AU 9456429	A1	19940908	AU 1994-56429	19940225
AU 676001	B2	19970227		
JP 07067661	A2	19950314	JP 1994-36026	19940307
US 5693757	A	19971202	US 1995-453265	19950530

PRIORITY APPLN. INFO.: US 1993-27498 19930305
US 1993-85000 19930701
US 1994-246982 19940520

AB A novel gene, huntingtin or IT15, that encodes the huntingtin protein and that shows a trinucleotide (CAG) repeat polymorphism and expansion mutation in Huntington's disease is cloned and characterized and shown to be the gene mapping to 4p16.3 that is assocd. with Huntington's disease. Uses of the gene and gene product in the diagnosis and treatment of Huntington's disease are also described. The gene was cloned by exon trapping and the cloned gene used to investigate the role of the trinucleotide repeat in the etiol. of the disease. There is considerable variation in the length of the repeat with only comparatively long repeats assocd. with the disease. The repeat length is unstable within a given Huntington's disease pedigree and this appears to be particularly the case for the paternal chromosome. The length of the repeat appeared to have some value in predicting the age of onset and severity of the disease.

IT **147617-90-1**, GenBank L12392
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; huntingtin gene IT15 affected by trinucleotide expansion mutation in Huntington's disease and its uses)

L30 ANSWER 17 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:568317 HCAPLUS
DOCUMENT NUMBER: 127:230356
TITLE: cDNAs containing trinucleotide repeats from human and primers for diagnosis of trinucleotide repeat diseases
INVENTOR(S): Neri, Christian; Cann, Howard M.; Cohen, Daniel
PATENT ASSIGNEE(S): Fondation Jean Dausset-Ceph, Fr.; Neri, Christian; Cann, Howard M.; Cohen, Daniel
SOURCE: PCT Int. Appl., 18 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: French
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9730178	A2	19970821	WO 1997-FR297	19970217
WO 9730178	A3	19971016		
W: CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
FR 2745007	A1	19970822	FR 1996-1864	19960215
FR 2745007	B1	19980507		
CA 2246362	AA	19970821	CA 1997-2246362	19970217

EP 894144 A2 19990203 EP 1997-905219 19970217
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
JP 2000505293 T2 20000509 JP 1997-529061 19970217
PRIORITY APPLN. INFO.: FR 1996-1864 19960215
WO 1997-FR297 19970217

AB A series of cDNAs that have a high level of CAG or CTG repeat codons are identified and primers suitable for identification of polymorphism or expansion of the trinucleotide repeats are described. The sequences are particularly useful for diagnosing trinucleotide repeat diseases. Natural polymorphism of the repeats is found in all of the sequences reported with up to 15 alleles obsd.

IT **164749-16-0**, GenBank T85390 **195330-76-8**
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; cDNAs contg. trinucleotide repeats from human and primers for diagnosis of trinucleotide repeat diseases)

L30 ANSWER 18 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:436078 HCAPLUS
DOCUMENT NUMBER: 127:44975
TITLE: Treatment and diagnosis of neurodegenerative diseases associated with polyglutamine tract-containing proteins using an antibody to polyglutamine
INVENTOR(S): Tora, Lazslo; Lutz, Yves; Trottier, Yvon; Mandel, Jean-louis
PATENT ASSIGNEE(S): Centre National De La Recherche Scientifique (Cnrs), Fr.; Institut National De La Sante Et De La Recherche Medicale (Inserm); Tora, Lazslo; Lutz, Yves; Trottier, Yvon; Mandel, Jean-Louis
SOURCE: PCT Int. Appl., 68 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: French
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9717445	A1	19970515	WO 1996-FR1773	19961108
W: CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
FR 2741088	A1	19970516	FR 1995-13576	19951110
FR 2741088	B1	19980130		

PRIORITY APPLN. INFO.: FR 1995-13576 19951110

AB A monoclonal antibody that recognizes a glutamine-rich peptide of TATA-binding protein can be used to treat and diagnose neurodegenerative diseases related to the presence of polyglutamine chains by means of a 1C2 antibody are disclosed. Methods can include gene therapy using the gene for a single-chain deriv. of the antibody. The antibody was shown to bind polyglutamine tracts with the strength of the binding proportional to the length of the polyglutamine domain. A polyglutamine epitope-contg. protein of 100 kDa (probably ataxin 1) was found to be assocd. with type 1 spinocerebellar ataxia (SCA). Four such proteins were found to be specific to type 3 (SCA). These proteins were found in the cytoplasm, whereas the polyglutamine epitope-contg. protein found in type 2 SCA was found in the nucleoplasm. A cDNA for this protein was cloned by antibody screening of a cDNA bank from a patient. Using these clones, the size of the polyglutamine repeats in patients could be detd. and a relationship between repeat size and the age of onset of the disease could be detd.

IT **191114-99-5**

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence, identification of **polymorphisms** and disease susceptibility using; treatment and diagnosis of neurodegenerative diseases assocd. with polyglutamine tract-contg. proteins using antibody to polyglutamine)

L30 ANSWER 19 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:424458 HCAPLUS
DOCUMENT NUMBER: 125:134181
TITLE: Survey of CAG/CTG repeats in human cDNAs representing new genes: candidates for inherited neurological disorders
AUTHOR(S): Neri, Christian; Albanese, Veronique; Lebre, Anne-Sophie; Holbert, Sebastien; Saada, Claudine; Bougueleret, Lydie; Meier-Ewert, Sebastian; Le Gall, Isabelle; Millasseau, Philippe; et al.
CORPORATE SOURCE: Fondation Jean-Dausset-CEPH, Paris, 75010, Fr.
SOURCE: Hum. Mol. Genet. (1996), 5(7), 1001-1009
CODEN: HMGEE5; ISSN: 0964-6906
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Expansion of polymorphic CAG and CTG repeats in transcripts is the cause of 6 inherited neurodegenerative or neuromuscular diseases and may be involved in several other genetic disorders of the central nervous system. To identify new candidate genes, we have undertaken a large-scale screening project for CAG and CTG repeats in human ref. cDNAs. We screened 100,128 brain cDNAs by hybridization. We also scanned GenBank expressed sequence tags for the presence of long CAG/CTG repeats in the extremities of cDNAs from several human tissues. Of the selected clones, 286 were found to represent new genes, and 72 have thus far been shown to contain CAG/CTG repeats. Our data indicate that CAG/CTG repeated 10 or more times are more likely to be polymorphic, and that new 3'-directed cDNAs with such repeats are very rare (1/2862). Nine new cDNAs contg. polymorphic (obsd. heterozygote frequency: 0.05-0.90) CAG/CTG repeats have been currently identified in cDNAs. All of the cDNAs have been assigned to chromosome, and 6 of them could be mapped with YACs to 1q32-q41, 3p14, 4q28, 3p21 and 12q13.3, 13q13.1-q13.2, and 19q13.43. Three of these clones are highly polymorphic and represent the most likely candidate genes for inherited neurodegenerative diseases and, perhaps, neuropsychiatric disorders of multifactorial origin.
IT **164749-16-0**, GenBank T85390
RL: PRP (Properties)
(nucleotide sequence; of human genes with **polymorphic** CAG/CTG repeats that may cause inherited neurol. disorders)

L30 ANSWER 20 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:133862 HCAPLUS
DOCUMENT NUMBER: 124:195621
TITLE: Development of a screening set for new (CAG/CTG)n dynamic mutations
AUTHOR(S): Gastier, Julie M.; Brody, Thomas; Pulido, Jacqueline C.; Businga, Thomas; Sunden, Sara; Hu, Xintong; Maitra, Shanak; Buetow, Kenneth H.; Murray, Jeffrey C.; et al.
CORPORATE SOURCE: Dep. of Genetics, Howard Hughes Medical Inst., Boston, MA, 02115, USA
SOURCE: Genomics (1996), 32(1), 75-85
CODEN: GNMCEP; ISSN: 0888-7543
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The expansion of a (CAG/CTG)n triplet repeat has been found to be assocd. with .gtoreq.7 genetic diseases, suggesting that this mechanism of disease

may be fairly common. To accelerate the discovery of new loci contg. (CAG/CTG)n triplet expansions, numerous genomic clones contg. this class of repeats were isolated. This study developed 338 sequence-tagged sites (STSs) contg. (CAG/CTG)n repeat sequences. Two hundred ninety-nine STSs were unambiguously assigned to chromosomes, and 89 of the total were assigned to YACs. The 141 STS that were developed based on (CAG/CTG)n repeats of .gtoreq.7 units were genotyped on 4 ref. CEPH individuals to est. their polymorphic quality.

IT **168230-47-5**, GenBank G07964 **168250-54-2**, GenBank G10010
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; screening set for (CAG/CTG)n repeat dynamic mutations in human genome)

L30 ANSWER 21 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:417904 HCAPLUS
DOCUMENT NUMBER: 123:26894
TITLE: Structural analysis of the 5' region of mouse and human Huntington disease genes reveals conservation of putative promoter region and di- and trinucleotide **polymorphisms**
AUTHOR(S): Lin, Biaoyang; Nasir, Jamal; Kalchman, Michael A.; McDonald, Helen; Zeisler, Jutta; Goldberg, Y. Paul; Hayden, Michael R.
CORPORATE SOURCE: Dep. Medical Genetics, University British Columbia, British Colombia, V6T 1Z4, Can.
SOURCE: Genomics (1995), 25(3), 707-15
CODEN: GNMCEP; ISSN: 0888-7543
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We have previously cloned and characterized the murine homolog of the Huntington disease (HD) gene and shown that it maps to mouse chromosome 5 within a region of conserved synteny with human chromosome 4p16.3. Here we present a detailed comparison of the sequence of the putative promoter and the organization of the 5' genomic region of the murine (Hdh) and human HD genes encompassing the first five exons. We show that in this region these two genes share identical exon boundaries, but have different-size introns. Two dinucleotide (CT) and one trinucleotide intronic polymorphism in Hdh and an intronic CA polymorphism in the HD gene were identified. Comparison of 940-bp sequence 5' to the putative translation start site reveals a highly conserved region (78.8% nucleotide identity) between Hdh and the HD gene from nucleotide -56 to -206 (of Hdh). Neither Hdh nor the HD gene have typical TATA or CCAAT elements, but both show one putative AP2 binding site and numerous potential Sp1 binding sites. The high sequence identity between Hdh and the HD gene for approx. 200 bp 5' to the putative translation start site indicates that these sequences may play a role in regulating expression of the Huntington disease gene.

IT **159200-17-6**, GenBank L34020
RL: PRP (Properties)
(nucleotide sequence; of mouse and human Huntington disease gene 5' regions reveals conservation of putative promoter region and di- and trinucleotide **polymorphisms**)

L30 ANSWER 22 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:125840 HCAPLUS
DOCUMENT NUMBER: 122:2791
TITLE: The Huntingtin gene and gene product and their use in the diagnosis and treatment of Huntington's disease
INVENTOR(S): Macdonald, Marcy E.; Ambrose, Christine M.; Duyao, Mabel P.; Gusella, James F.
PATENT ASSIGNEE(S): General Hospital Corp, USA
SOURCE: Eur. Pat. Appl., 66 pp.

CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 614977	A2	19940914	EP 1994-301587	19940307
EP 614977	A3	19960228		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
CA 2116280	AA	19940906	CA 1994-2116280	19940223
AU 9456429	A1	19940908	AU 1994-56429	19940225
AU 676001	B2	19970227		
JP 07067661	A2	19950314	JP 1994-36026	19940307

PRIORITY APPLN. INFO.: US 1993-27498 19930305
US 1993-85000 19930701

AB A novel gene, huntingtin, and the protein encoded by it are described and their role in Huntington's disease studied. The protein and the gene are useful in the diagnosis and treatment of Huntington's disease. Exons from the proximal region contiguous to D4S127 were cloned by trapping methods and a full-length cloned obtained by walking. An unstable (polymorphic) trinucleotide repeat of the codon CAG was found with 17 alleles showing 11-34 repeats found in normal alleles of the gene. An allele assocd. with Huntington's disease had a 48-fold repeat; alleles assocd. with the disease had a larger no. of repeats than did those not assocd. with the disease.

IT **159447-38-8**
RL: BOC (Biological occurrence); BPR (Biological process); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PROC (Process); USES (Uses)
(nucleotide sequence; the Huntingtin gene and gene product and their use in the diagnosis and treatment of Huntington's disease)

L30 ANSWER 23 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1993:402002 HCAPLUS
DOCUMENT NUMBER: 119:2002
TITLE: The nucleotide sequence of the .alpha./.beta.-type gliadin gene from tetraploid wheat (Triticum timofeevi)
AUTHOR(S): Filatov, V. D.; Kaliev, A. B.; Zairov, S. Z.
CORPORATE SOURCE: Inst. Mol. Biol. Biokhim., Kazakhstan
SOURCE: Izv. Akad. Nauk Resp. Kaz., Ser. Biol. (1992), (1), 40-3
CODEN: IKABEV
DOCUMENT TYPE: Journal
LANGUAGE: Russian

AB The genomic clone encoding an .alpha./.beta. type gliadin was isolated from a tetraploid wheat genomic library and the entire DNA sequence of this clone was detd. The clone differs from the analogous .alpha./.beta. type gliadin genes of hexaploid wheat (clone pw8233) in general positions within the coding region; in particular there are 9 nucleotide changes, 5 of which change the encoded amino acid sequence. A substitution at nucleotide 776 results in a substitution of glutamine for leucine, an insertion of AGC at nucleotides 974-6 results in the addn. of a glutamine residue, and a substitution of C by T at nucleotide 1342 results in the substitution of leucine for phenylalanine. The 5' region of the gene contains a TATA and a CCAAT box. The 5' flanking region also contains the tissue-specific enhancer, element 300, found in the majority of prolamin genes. The 3' flanking region contains a translation terminator and 2 polyadenylation signals.

IT **147604-61-3**, Deoxyribonucleic acid (Triticum timopheevi clone **gT1**.9 .alpha./.beta.-gliadin gene plus 5'- and 3'-flanking region

fragment)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

L30 ANSWER 24 OF 24 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1991:486767 HCAPLUS
DOCUMENT NUMBER: 115:86767
TITLE: Genetic length **polymorphism** determination by polymerase chain reaction
INVENTOR(S): Jaeckle, Herbert; Tautz, Diethard
PATENT ASSIGNEE(S): Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V., Fed. Rep. Ger.
SOURCE: Ger. Offen., 9 pp.
CODEN: GWXXBX
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 3834636	A1	19900419	DE 1988-3834636	19881011
DE 3834636	C2	19920220		
WO 9004040	A1	19900419	WO 1989-EP1203	19891011
W: JP, US				
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
EP 438512	A1	19910731	EP 1989-912096	19891011
EP 438512	B1	19971229		
R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
JP 04501207	T2	19920305	JP 1989-511152	19891011
JP 3218318	B2	20011015		
AT 161585	E	19980115	AT 1989-912096	19891011
US 5766847	A	19980616	US 1993-145617	19931104
PRIORITY APPLN. INFO.:			DE 1988-3834636 A	19881011
			WO 1989-EP1203 W	19891011
			US 1991-681494 B1	19910610

AB Genetic length polymorphisms are detected using polymerase chain reaction (PCR) using primers that flank the possible polymorphic region. The length polymorphism of a simple DNA sequence comprising predominantly repetitive CAG in Drosophila DNA was analyzed for polymorphism.
IT **135373-39-6**, Deoxyribonucleic acid (Drosophila melanogaster repetitive fragment)
RL: PRP (Properties)
(length **polymorphism** of, detection of, with polymerase chain reaction)

=> sel hit rn l30 1-24
E1 THROUGH E31 ASSIGNED

– hit Registry #'s selected out of the preceeding citations, crossed back into Registry, & combined with original seq. search answer set

=> d his l31

(FILE 'HCAPLUS' ENTERED AT 12:25:12 ON 04 DEC 2001)
SEL HIT RN L30 1-24

FILE 'REGISTRY' ENTERED AT 12:27:30 ON 04 DEC 2001
L31 31 S L2 AND E1-E31

=> d rn cn sql kwic nte l31 1-31

L31 ANSWER 1 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **300736-74-7** REGISTRY – Use Registry # to match sequence to citation
CN DNA (human gene AR single nucleotide polymorphism-containing fragment)

(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 46: PN: WO0058519 FIGURE: 5 claimed DNA
SQL 598 SQL = sequence length

SEQ 201 tttgctgctg ctgcagcagc agcagcagca gcagcagcag cagcagcagc

251 agcagcagca gcagcagcag cagcaagaga ctagccccag gcagcagcag

HITS AT: 232-276
NTE doublestranded

L31 ANSWER 2 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **300736-73-6** REGISTRY
CN DNA (human gene AR single nucleotide polymorphism-containing fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 45: PN: WO0058519 FIGURE: 5 claimed DNA
SQL 598

SEQ 201 tttgctgctg ctgcagcagc agcagcagca gcagcagcag cagcagcagc

251 agcagcagca gcagcagcag cagcaagaga ctagccccag gcagcagcag

HITS AT: 232-276
NTE doublestranded

L31 ANSWER 3 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **252869-02-6** REGISTRY
CN 3: PN: WO9966059 SEQID: 3 unclaimed DNA (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AX008545
SQL 375

SEQ 251 aaagaaaaat tgccaacaac agcagcagca gcagcagcag cagcagcaac

HITS AT: 264-299
NTE doublestranded

L31 ANSWER 4 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **249928-12-9** REGISTRY
CN DNA (human chromosome Xq13 gene HOPA protein cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9955915 SEQID: 2 claimed DNA
SQL 6764

SEQ 6251 gcagatcctg cggcagcagc agcaacagca acagcagcag cagcagcagc

6301 agcaacagca acagcagcag caacaacagc aacaccagca gcaacagcag

HITS AT: 6276-6305
NTE doublestranded

L31 ANSWER 5 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **249928-10-7** REGISTRY
CN DNA (human clone PCTG4 gene HOPA plus neuroligin-3 gene plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9955915 SEQID: 1 claimed DNA
SQL 54548

SEQ 23851 tctgaagtat cttttgtgtt cttatagcag cagcagcaac agcaacagca

```
                                                                  = ==========
     23901 gcagcagcag cagcagcaac agcaacagca gcagcagcaa cagcaacaac
           ========== =========
HITS AT:    23890-23919
NTE  doublestranded

L31  ANSWER 6 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   249726-48-5  REGISTRY
CN   PN: WO9955915 FIG: 5 unclaimed DNA (9CI)  (CA INDEX NAME)
SQL  254

SEQ    101 caacagcaac agcagcagca gcagcagcag caacagcaac agcagcagca
           ======= ========== ========== ===
HITS AT:    104-133
NTE  doublestranded

L31  ANSWER 7 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   244017-45-6  REGISTRY
CN   PN: WO9945944 SEQID: 14 unclaimed DNA (9CI)  (CA INDEX NAME)
SQL  10348

SEQ    351 gtccctcaag tccttccagc agcagcagca gcagcagcag cagcagcagc
                                                   === ==========
       401 agcagcagca gcagcagcag cagcagcagc aacagccgcc accgccgccg
           ========== ========== ========== ==
HITS AT:    388-432
NTE  doublestranded

L31  ANSWER 8 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   237745-29-8  REGISTRY
CN   DNA (Rattus rattus olfactory epithelium potassium channel-specifying cDNA)
     (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AX018992
SQL  3112

SEQ   1601 gcagcagccg caacagcaac aacagcagca acagcagcag cagcagcagc
                                 ===== ========== ==========
      1651 agcaacaaca acagcagcag caacagccac agacacctgg tagttccaca
           =====
HITS AT:    1626-1655
NTE  doublestranded

L31  ANSWER 9 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   228686-91-7  REGISTRY
CN   DNA (human clone 7B3/CTG-4 gene HOPA plus flanks) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   5051: PN: WO0153836 TABLE: 3-3 claimed DNA
CN   DNA (human gene OPA plus flanks)
CN   DNA (human OPA-containing protein gene OPA plus flanks)
CN   GenBank AF132033
SQL  25187

SEQ  23851 tgaagtatct tttgtgttct tatagcagca gcagcaacag caacagcagc
                                                   === ==========
     23901 agcagcagca gcagcaacag caacagcagc agcagcaaca gcaacaacag
           ========== =======
HITS AT:    23888-23917
NTE  doublestranded

L31  ANSWER 10 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   225458-12-8  REGISTRY
CN   DNA (human chromosome 1q32-q41 clone 55i10 90429-nucleotide fragment)
```

(9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA (human clone WO0118542_SEQID_6765 ovary tumor-associated protein cDNA)
CN GenBank AL035408
CN PN: WO0118542 SEQID: 6765 claimed DNA
SQL 90429

SEQ 57051 accgccacca ccgccgccgc caccaccgta gcagcagcag cagcagcagc
57101 agcagcagca gcagcagcaa gagtaactct gacttaggaa tagagacagc
HITS AT: 57082-57120
NTE doublestranded

L31 ANSWER 11 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **224698-76-4** REGISTRY
CN DNA (human huntingtin cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AB016794
SQL 13467

SEQ 201 agcagcagca gcagcagcag cagcagcagc agcagcagca gcagcagcag
251 cagcagcagc aacagccgcc accgccgccg ccgccgccgc cgcctcctca
HITS AT: 218-262
NTE singlestranded

L31 ANSWER 12 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **224698-75-3** REGISTRY
CN DNA (miniature swine huntingtin gene cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA (miniature swine strain CSK-goettingen huntingtin cDNA plus flanks)
CN GenBank AB016793
CN GenBank E26529
SQL 12749

SEQ 151 gaaagctttc gagtctctca agtccttcca gcagcagcag cagcaacagc
201 agcagcagca gcagcagcag cagcaacagc agctgccgcc accgccgcct
HITS AT: 191-226
NTE singlestranded

L31 ANSWER 13 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **222771-68-8** REGISTRY
CN DNA (human gene OPA dodecamer insertion-containing fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA (human protein OPA (opposite paired domain-containing) gene OPA dodecamer insertion-containing fragment)
CN GenBank AF071311
SQL 253

SEQ 101 caacagcaac agcagcagca gcagcagcag caacagcaac agcagcagca
HITS AT: 104-133
NTE doublestranded

L31 ANSWER 14 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **221891-82-3** REGISTRY
CN DNA (human clone GCT10D04 gene GT1 plus flanks) (9CI) (CA INDEX NAME)

OTHER NAMES:
CN GenBank AX004680
SQL 6022

SEQ 1301 cgggccgcct cagctatgac cagcagcagc agcagcagca gcagcagcag
1351 cagcagcagc aagcccttca gagccggcac catgcccagg aaaccctcca
HITS AT: 1321-1362
NTE doublestranded

L31 ANSWER 15 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **212951-28-5** REGISTRY
CN DNA (human gene OPA protein OPA (opposite paired domain-containing) cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4954: PN: WO0153836 TABLE: 3-3 claimed DNA
CN DNA (human gene OPA OPA-containing protein cDNA plus flanks)
CN GenBank AF071309
SQL 6788

SEQ 6251 agcagcagca gcagcagatc ctgcggcagc agcagcaaca gcaacagcag
6301 cagcagcagc agcagcaaca gcaacagcag cagcagcaac agcaacaaca
HITS AT: 6289-6318
NTE singlestranded

L31 ANSWER 16 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **208229-17-8** REGISTRY
CN DNA (human chromosome 17-specific CAG repetitive region Dir1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AB009843
SQL 1410

SEQ 1251 cagcagcagc agcagcagca gcagcagcag cagcagcagc agcagcagca
1301 gcagcagcag cagcagcagc agcagcagca gcagcaaaag accttccttc
HITS AT: 1293-1337
NTE doublestranded

L31 ANSWER 17 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **206322-26-1** REGISTRY
CN DNA (human clone ctg-17 STS (sequence tag site)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF021111
SQL 274

SEQ 51 cccggccact gcagtcttct gccctgctgg acagcagcag cagcagcagc
101 agcagcagca gcagcagcag caacagtaac agcagcagtt cgaccggacc
HITS AT: 82-123
NTE doublestranded

L31 ANSWER 18 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **206322-20-5** REGISTRY
CN DNA (human STS (sequence tag site) 221-nucleotide fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF021105

```
SQL  221

SEQ    101 aacaaacaac agcagcagca gcagcagcag cagcagcagc agcagcaatg
                ==== ========== ========== ========== ========

HITS AT:   107-148
NTE  doublestranded

L31  ANSWER 19 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   201441-24-9  REGISTRY
CN   DNA (Mus musculus strain C57BL/6J brain gene Bcng-1 ion channel BCNG-1
     (brain cyclic nucleotide gated 1) cDNA plus 3'-flank) (9CI)  (CA INDEX
     NAME)
OTHER NAMES:
CN   DNA (mouse strain C57BL/6J brain gene Bcng-1 glycoprotein BCNG-1 cDNA plus
     3'-flank)
CN   GenBank AF028737
SQL  3305

SEQ   2201 cagactcaga ctcagactca gcagcagcag cagcaacagc agcagcagca
                                           ========== ==========

      2251 gcagcagcaa cagcaacaac agcagcagca gcagcagcag cagcagcagc
           ==========
HITS AT:   2231-2260
NTE  singlestranded

L31  ANSWER 20 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   200048-64-2  REGISTRY
CN   DNA (Canis familiaris gene DRPLA fragment) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   DNA (dog gene DRPLA dentatorubro-pallidoluysian atrophy protein fragment)
CN   GenBank AF030429
SQL  324

SEQ    101 agccgccgcc gcagtcgcag cagcgaccgc agcagcagca gcagcagcag
                                        = ========== ==========

       151 cagcagcagc agcagcagca acagcatcat gggagctctg ggccccctcc
           ========== ========== = 
HITS AT:   130-171
NTE  doublestranded

L31  ANSWER 21 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   195330-76-8  REGISTRY
CN   DNA (human clone 2.116 trinucleotide repeat-containing EST (expressed
     sequence tag)) (9CI)  (CA INDEX NAME)
SQL  2226

SEQ     51 ggccagcctc aggtagcagc agcagcagca gcagcagcag cagcagcagc
                                              ======= ==========

       101 agcagcagca gcagcagcag cagcagcaat gtttcacttc ttcagaaagc
           ========== ========== =========
HITS AT:   85-129
NTE  doublestranded

L31  ANSWER 22 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   191114-99-5  REGISTRY
CN   DNA (human clone DAN15 spinocerebellar ataxia-associated
     polyglutamine-containing antigen-specifying) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank A62703
SQL  54

SEQ      1 cagcagcagc agcagcagca gcaacagcag cagcagcagc agcagcaaca
                           == ========== ========== ========

                    Searched by Barb O'Bryen STIC  308-4291
```

HITS AT: 19-48
NTE doublestranded

L31 ANSWER 23 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **168250-54-2** REGISTRY
CN DNA (human STS (sequence-tagged site) GCT16E06.P18287) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human sequence tag site GCT16E06.P18287)
OTHER NAMES:
CN GenBank G10010
SQL 274

SEQ 51 ctggagcagg agcagcagga gcagcagcag cagcagcagc agcagcagca
========= ========== ==========
101 gcagcagcag caattatcag caaagccttt gttaatgagc agtgttttta
========== ===
HITS AT: 72-113
NTE doublestranded

L31 ANSWER 24 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **168230-47-5** REGISTRY
CN DNA (human STS (sequence-tagged site) GCT8D06.P11190) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human sequence tag site GCT8D06.P11190)
OTHER NAMES:
CN GenBank G07964
SQL 470

SEQ 1 tgacctcaca taaagcaagg tggctggcag agtccaccgt tctatgcagc
====
51 agcagcagca gcagcagcag cagcaaccat cacttgtcgt tcgatgtgtt
========== ========== ======
HITS AT: 47-76
NTE doublestranded

L31 ANSWER 25 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **164749-16-0** REGISTRY
CN DNA (human clone 114128 CAG/CTG repeat-containing fragment) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human clone 114128 CAG/CTG repeat-containing fragment)
OTHER NAMES:
CN 401: PN: WO0123426 TABLE: 3 claimed DNA
CN DNA (human clone 114128 3'-expressed sequence tag cDNA)
CN DNA (human clone 114128 EST (expressed sequence tag))
CN GenBank. . .

SEQ 101 tacatgtcag gaaactgtgg agcctccgca gactctccac cagcagcagc
==========
151 agcagcagca gcagcagcag caagagaagc ttccaattag ggcaggggt
========== ========== ===
HITS AT: 141-173
NTE singlestranded

L31 ANSWER 26 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **159447-38-8** REGISTRY
CN DNA (human clone L1C2 gene huntingtin protein cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human clone L1C2 gene huntingtin protein messenger

RNA-complementary plus 5'- and 3'-flanking region fragment)
OTHER NAMES:
CN DNA (human clone L1C2 IT15 cDNA plus 5'- and 3'-flanking region fragment)
SQL. . .

SEQ 351 gtccctcaag tccttccagc agcagcagca gcagcagcag cagcagcagc
=== ==========

401 agcagcagca gcagcagcag cagcagcagc aacagccgcc accgccgccg
========== ========== ========== ==

HITS AT: 388-432
NTE doublestranded

L31 ANSWER 27 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **159200-17-6** REGISTRY
CN DNA (human clone L191F1 gene HD exon 1 plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human clone L191F1 gene HD exon 1 plus 5'- and 3'-flanking region fragment)
OTHER NAMES:
CN DNA (human gene HD promoter region plus exon 1 fragment)
CN GenBank L34020
SQL 4105

SEQ 3651 cagcagcagc agcagcagca gcagcagcag cagcagcagc agcaacagcc
========== ========== ========== ========== =====

HITS AT: 3651-3695
NTE doublestranded

L31 ANSWER 28 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **147617-90-1** REGISTRY
CN DNA, (human clone IT16C/IT16B/IT15B gene IT15 protein cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, (human clone IT16C/IT16B/IT15B gene IT15 protein messenger RNA-complementary plus 5'- and 3'-flanking region fragment)
OTHER NAMES:
CN 190: PN: WO0157188 SEQID: 490 claimed DNA
CN DNA (human clone WO157188-SEQID-490 protein fragment-specifying. . .

SEQ 351 gtccctcaag tccttccagc agcagcagca gcagcagcag cagcagcagc
=== ==========

401 agcagcagca gcagcagcag cagcagcagc aacagccgcc accgccgccg
========== ========== ========== ==

HITS AT: 388-432

L31 ANSWER 29 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **147604-61-3** REGISTRY
CN DNA (Triticum timopheevi clone gT1.9 .alpha./.beta.-gliadin gene plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (Triticum timopheevi clone gT1.9 .alpha./.beta.-gliadin gene plus 5'- and 3'-flanking region fragment)
SQL 1648

SEQ 901 ccgcaaccac agtattcgca accacaacaa ccaatttcac agcaacagca
= ==========

951 gcagcagcag cagcagcaac aacagcaaca acaacaacaa caacaaatcc
========== ==========

HITS AT: 940-969
NTE doublestranded

L31 ANSWER 30 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN **140026-49-9** REGISTRY

```
CN   PN: WO9945943 SEQID: 10 unclaimed DNA (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AR153576
CN   GenBank M23263
SQL  3715

SEQ    701 tgcagcagca gcagcagcag cagcagcagc agcagcagca gcagcagcag
                  == ========== ========== ========== ==========
       751 caagagacta gccccaggca gcagcagcag cagcagggtg aggatggttc
           ===
HITS AT:   709-753
NTE  singlestranded

L31  ANSWER 31 OF 31  REGISTRY  COPYRIGHT 2001 ACS
RN   135373-39-6  REGISTRY
CN   DNA (Drosophila melanogaster repetitive element fragment) (9CI)  (CA INDEX
     NAME)
OTHER CA INDEX NAMES:
CN   Deoxyribonucleic acid (Drosophila melanogaster repetitive element
     fragment)
SQL  379

SEQ    101 ccagcaacag cagcagcagc agcagcagca acagcagcaa catcagcagc
           ========== ========== ========== =
HITS AT:   102-131
NTE  doublestranded


=> fil hom
FILE 'HOME' ENTERED AT 12:30:45 ON 04 DEC 2001
```